

1 GCGGCCGCGAATTCGGCACCAGGGGCGCTCTCTCCCGGTGTGGGTACTGCTGTCTGTGGT 60
 -----+-----+-----+-----+-----+-----+-----+
 61 GTGGCTGTGGGACCCGTGAGCAAGCAGCGACGCCAGCGGCGGAGAACCGACGAAAGGTGT 120
 -----+-----+-----+-----+-----+-----+-----+
 121 CACCACAGTGATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCC 180
 -----+-----+-----+-----+-----+-----+-----+
 MetAlaValGluAspSerThrLeuGlnValValValArgValArgProPr
 181 CACCCCTCGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGT 240
 -----+-----+-----+-----+-----+-----+-----+
 oThrProArgGluLeuAspSerGlnArgArgProValValGlnValValAspGluArgVa
 241 GCTGGTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCTTGGCCTGAAATGGGGTGGCAC 300
 -----+-----+-----+-----+-----+-----+-----+
 lLeuValPheAsnProGluGluProAspGlyGlyPheProGlyLeuLysTrpGlyGlyTh
 301 CCATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTTGG 360
 -----+-----+-----+-----+-----+-----+-----+
 rHisAspGlyProLysLysLysGlyLysAspLeuThrPheValPheAspArgValPheGl
 361 CGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGACAGCTT 420
 -----+-----+-----+-----+-----+-----+-----+
 yGluAlaAlaThrGlnGlnAspValPheGlnHisThrThrHisSerValLeuAspSerPh
 421 CCTCCAGGGCTACAACCTGCTCAGTGTTCCTACGGGGGCCACCGGGGCTGGGAAGACACA 480
 -----+-----+-----+-----+-----+-----+-----+
 eLeuGlnGlyTyrAsnCysSerValPheAlaTyrGlyAlaThrGlyAlaGlyLysThrHi
 481 CACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACCGTGGAAGTGT 520
 -----+-----+-----+-----+-----+-----+-----+
 sThrMetLeuGlyArgGluGlyAspProGlyIleMetTyrLeuThrThrValGluLeuTy
 541 CAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTCATCAGCTACCAGGA 600
 -----+-----+-----+-----+-----+-----+-----+
 rArgArgLeuGluAlaArgGlnGlnGluLysHisPheGluValLeuIleSerTyrGlnGl

FIG. 1A

601 GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCTTGCCATCCGCGA 660
 -----+-----+-----+-----+-----+-----+
 uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgGl

 661 GGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA 720
 -----+-----+-----+-----+-----+-----+
 uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaGl

 721 GCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC 780
 -----+-----+-----+-----+-----+-----+
 uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAl

 781 CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTTGTGAAGCAGCAGGACCG 840
 -----+-----+-----+-----+-----+-----+
 aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspAr

 841 GGTTCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG 900
 -----+-----+-----+-----+-----+-----+
 gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaGl

 901 CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGGAGCGGCTGCGGGAGGGGGCCAACAT 960
 -----+-----+-----+-----+-----+-----+
 ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIl

 961 CAACCGCTCTCTGCTGGCGCTCATCAACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCG 1020
 -----+-----+-----+-----+-----+-----+
 eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyAr

 1021 CAAGACCCATGTGCCCTACCGGGACAGCAAAGTACCCGCTGCTCAAAGACTCCCTCGG 1080
 -----+-----+-----+-----+-----+-----+
 gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuGl

 1081 GGGCAACTGCCGCACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA 1120
 -----+-----+-----+-----+-----+-----+
 yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAs

 1141 CACGTACAACACCCTCAAATATGCCGACCGGG**GCCA**AGGAGATCAGGCTCTCGCTGAAGAG 1200
 -----+-----+-----+-----+-----+-----+
 pThrTyrAsnThrLeuLysTyrAlaAspArg**Ala**LysGluIleArgLeuSerLeuLysSe

 1201 CAATGTGACCAGCCTGGACTGTCACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA 1260
 -----+-----+-----+-----+-----+-----+
 rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuGl

FIG. 1B

1261 GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCC 1320
 -----+-----+-----+-----+-----+-----+ 1320
 nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

1321 ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC 1380
 -----+-----+-----+-----+-----+-----+ 1380
 oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

1381 CCCCTTGCCACCCACCCCTCCCAGCCAGCCCTGCACCCCAGAGCTCCCTGCAGGGCCTAG 1440
 -----+-----+-----+-----+-----+-----+ 1440
 rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

1441 AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCAGGTGGAGAGGGCCATGGAAGGGAA 1500
 -----+-----+-----+-----+-----+-----+ 1500
 gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

1501 CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCAGCTGAGGAGGTTCC 1560
 -----+-----+-----+-----+-----+-----+ 1560
 nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

1561 AACCCAGATGCCAGAGCAGAACCCACACATGCACTGCCAGAGTCCCCTCGCCTGACCCT 1620
 -----+-----+-----+-----+-----+-----+ 1620
 oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

1621 GCAGCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAAGTGGATGGGGACCGTTCTAA 1680
 -----+-----+-----+-----+-----+-----+ 1680
 uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

1681 GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCAGCGGCAGTACTCCCTGCTCCAAGCAGC 1740
 -----+-----+-----+-----+-----+-----+ 1740
 sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

1741 CAACCTCCTGACGCCCCGACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA 1800
 -----+-----+-----+-----+-----+-----+ 1800
 aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

1801 GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC 1860
 -----+-----+-----+-----+-----+-----+ 1860
 uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

1861 TCTGGCTCAGGAGCTGTGTTTCAGAGTCAATCCCTGTGCCGTCTCCTCTCTGCCAGAGCC 1920
 -----+-----+-----+-----+-----+-----+ 1920
 oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr

FIG. 1C

1921 TCCAGGATACACTGGCCCTGTGACCCGGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA 1980
 -----+-----+-----+-----+-----+-----+
 oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi

 1981 CACCCTGGGAATCCCGCCTGGACCCAACCTGCACCCCAGCCCAGGGGTCCCGATGGCCCAT 2040
 -----+-----+-----+-----+-----+-----+
 sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe

 2041 GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG 2100
 -----+-----+-----+-----+-----+-----+
 tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr

 2101 GGGCACCAAGCGCCAGCGCCAGTCCTTCCTGCCCTGCCTAAGGAGAGGGTCTCTGCCTGA 2160
 -----+-----+-----+-----+-----+-----+
 gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs

 2161 CACCCAACCTTCACAGGGGCCAGCACCCCCAAAGGAGAAAGGGCCTCCTCCCCCTGCCA 2220
 -----+-----+-----+-----+-----+-----+
 pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi

 2221 TTCCCCTCGCGTTTGCCCAGCCACAGTCATCAAAGCCGGGTGCCCTGGGCCCTTCCGC 2280
 -----+-----+-----+-----+-----+-----+
 sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl

 2281 CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACCTCGAGACCTCAATGCCACCTTTGA 2340
 -----+-----+-----+-----+-----+-----+
 aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs

 2341 TCTCTCTGAGGAGCCTCCCTCAAAGCCCAGTTTCCATGAATGCATTGGCTGGGACAAAAT 2400
 -----+-----+-----+-----+-----+-----+
 pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl

 2401 ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCTGT 2460
 -----+-----+-----+-----+-----+-----+
 eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh

 2461 CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA 2520
 -----+-----+-----+-----+-----+-----+
 eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy

 2521 GCGCGTTGCGAGTTCCTCAGTCTCCCATGGCCGAGCCGCATCGCCCGCCTCCCCAGCAG 2580
 -----+-----+-----+-----+-----+-----+
 sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe

FIG. 1D

2581 CACTTTGAAGAGGCCAGCTGGGCCCCTTG TACTCCCAGAGCTGCCCTTGAGTCCCCTGTG 2640
 -----+-----+-----+-----+-----+-----+-----+
 rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy

 2641 CCCTAGCAACCGGAGGAATGGAAAGGACCTCATCAGGGTGGGGAGAGCGCTCTCAGCAGG 2700
 -----+-----+-----+-----+-----+-----+-----+
 sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl

 2701 GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCCTGACCACCAAGGTGTCCTAAC 2760
 -----+-----+-----+-----+-----+-----+-----+
 yAsnGlyValThrLysValSer

 2761 CTACCGGCCCCTCTGCTGGATACCCCTCTTGGACCTGTAGCCACCTGCACCAGGAGCTGG 2820
 -----+-----+-----+-----+-----+-----+-----+

 2821 ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC 2880
 -----+-----+-----+-----+-----+-----+-----+

 2881 TCCCCAGACATCCATCCTGCTACTCACCCCTCTGTTAATCTCCTGTTACACTCAGCTTCTT 2940
 -----+-----+-----+-----+-----+-----+-----+

 2941 GGCATGTACATATTCATTTGTGAGTGTTAATGTGCTGCTGTTTTTTGTTTTTTGGTGTT 3000
 -----+-----+-----+-----+-----+-----+-----+

 3001 TTTGTTTTTTGTTTTTTTTGTTTTGAGATGGAGTCTTACTCTGTCGCCCAGGCTGGAGTG 3060
 -----+-----+-----+-----+-----+-----+-----+

 3061 CAGTGGTACGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGTAATTCTCCTGC 3120
 -----+-----+-----+-----+-----+-----+-----+

 3121 CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATCACCACACCCAGCTAATTTTCGT 3180
 -----+-----+-----+-----+-----+-----+-----+

 3181 CTTTTTAATAGAGAGGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC 3240
 -----+-----+-----+-----+-----+-----+-----+

 3241 AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC 3300
 -----+-----+-----+-----+-----+-----+-----+

 3301 CTGGCCCGTGTTGCTGTTTTTAAAGGTGCTGCCATGTTCCCCCATCTTTTTTTTTTTGAG 3360
 -----+-----+-----+-----+-----+-----+-----+

FIG. 1E

3361 ATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA 3420
 -----+-----+-----+-----+-----+-----+-----+
 3421 AGCTCCGCCTCCCAGGTTACACCATTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA 3480
 -----+-----+-----+-----+-----+-----+-----+
 3481 CAGGCGCCCAACCACGCGCCGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCAC 3540
 -----+-----+-----+-----+-----+-----+-----+
 3541 CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCCTCGGCCTCCCAAAG 3600
 -----+-----+-----+-----+-----+-----+-----+
 3601 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC 3660
 -----+-----+-----+-----+-----+-----+-----+
 3661 TGTGCAGGCAGACGGCTCTTGGGCTCTTTCCCCACCTGTCTCTAACACAGGCCCCACGG 3720
 -----+-----+-----+-----+-----+-----+-----+
 3721 TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTGCGGGAGCGGGGAGTCGCGGCT 3780
 -----+-----+-----+-----+-----+-----+-----+
 3781 TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA 3840
 -----+-----+-----+-----+-----+-----+-----+
 3841 CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTTCCAAATGAAGACAGCTTTA 3900
 -----+-----+-----+-----+-----+-----+-----+
 3901 TTGCTTAACTCTATTGTACATAGGATACACGTTTCAGTGTAATAAAGTGTAAGGGGAA 3960
 -----+-----+-----+-----+-----+-----+-----+
 3961 TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT 4020
 -----+-----+-----+-----+-----+-----+-----+
 4021 GATCCTTTATTTCTGCATATATATAGATATATACATATATTTTGGGTATAACAATAAA 4080
 -----+-----+-----+-----+-----+-----+-----+
 4081 CCGTCTCCATCCTTGGGAAAAAAAAAAAA 4108
 -----+-----+-----+-----+-----+-----+-----+

FIG. 1F



1 GACAGCACGC TGCAAGTAGT GGTACGGGTG CGGCCCCCA CCCCTCGGGA GCTGGACAGT
61 CAGCGGCGGC CAGTGGTTCA GGTGGTGGAC GAGCGGGTGC TGGTGTTTAA CCCTGAGGAG
121 CCCGATGGAG GGTTCCTTGG CCTGAAATGG GGTGGCACCC ATGATGGCCC CAAGAAGAAG
181 GGCAAAGACC TGACGTTTGT CTTTGACCGG GTCTTTGGCG AGGCGGCCAC CCAACAGGAC
241 GTGTTCCAGC ACACCACGCA CAGCGTCCTG GACAGCTTCC TCCAGGGCTA CAACTGCTCA
301 GTGTTTGCCT ACGGGGCCAC CGGGGCTGGG AAGACACACA CCATGCTGGG AAGGGAGGGG
361 GACCCCGGCA TCATGTACCT GACCACCGTG GAACTGTACA GGCGCCTGGA GGCCCGCCAG
421 CAGGAGAAGC ACTTCGAGGT GCTCATCAGC TACCAGGAGG TGTATAATGA ACAGATCCAT
481 GACCTCCTGG AGCCCAAGGG GCCCCTTGCC ATCCGCGAGG ACCCCGACAA GGGGGTGGTG
541 GTGCAAGGAC TTTCTTTCCA CCAGCCAGCC TCAGCCGAGC AGCTGCTGGA GATACTGACC
601 AGGGGGAACC GTAACCGCAC GCAGCACCCC ACTGATGCCA ACGCGACTTC CTCCCGCTCC
661 CATGCCATCT TCCAGATCTT TGTGAAGCAG CAGGACCGGG TTCCAGGACT GACCCAGGCT
721 GTCCAGGTGG CCAAGATGAG CCTGATTGAC CTGGCTGGCT CAGAGCGGGC ATCCAGCACC
781 CATGCGAAGG GGGAGCGGCT GCGGGAGGGG GCCAACATCA ACCGCTCTCT GCTGGCGCTC
841 ATCAACGTCC TCAATGCCTT GGCCGATGCA AAGGGCCGCA AGACCCATGT GCCCTACCGG
901 GACAGCAAAC TGACCCGCCT GCTCAAAGAC TCCCTCGGGG GCAACTGCCG CACAGTGATG
961 ATCGCTGCCA TCAGCCCCTC CAGCCTGACC TACGAGGACA CGTACAACAC CCTC

FIG. 2

1 DSTLQVVVRV RPPTPRELDS QRRPVVQVVD ERVLVFNPEE PDGGFPGLKW GGTHDGPKKK
61 GKDLTFVFDR VFGEAATQOD VFQHTTHSVL DSFLQGYNCS VFAYGATGAG KTHTMLGREG
121 DPGIMYLTTV ELYRRLEARQ QEKHFEVLIS YQEVYNEQIH DLLEPKGPLA IREDPDKGVV
181 VQGLSFHQPA SAEQLLEILT RGNRNRTQHP TDANATSSRS HAIFQIFVKQ QDRVPGLTQA
241 VQVAKMSLID LAGSERASST HAKGERLREG ANINRSLAL INVLNALADA KGRKTHVPYR
301 DSKLTRLLKD SLGGNCRTVM IAAISPSSLT YEDTYNTL

FIG. 3



MAVEDSTLQVVVRVPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT
HDGPKKKGKDLTFVFDRVFGAATQQDVFQHTTHSVLDSFLQGYNCSVFAYGATGAG
KTHTMLGREGDPGIMYLTVELYRRLEARQQEKHFEVLISYQEVYNEQIHDLLEPKG
PLAIREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAI F
QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLALI
NVLNALADAKGRKTHVPYRDSKLTRLLKDSLGGNCRTVMIAAISPSSTLYEDTYNTL
KYADRAKEIRLKGNSKLEGKPIPNPLLGLDSTRTGHHHHHH

FIG. 4

ATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCACCCT
CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGTGCTG
GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCTGGCCTGAAATGGGGTGGCACC
CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTT
GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC
AGCTTCCTCCAGGGCTACAACCTGCTCAGTGTTTGCCTACGGGGCCACCGGGGCTGGG
AAGACACACACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACC
GTGGAACGTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC
ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG
CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTC
CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC
CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC
CAGATCTTTGTGAAGCAGCAGGACCGGGTTCAGGACTGACCCAGGCTGTCCAGGTG
GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG
AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC
AACGTCCTCAATGCCTTGCCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG
GACAGCAAACCTGACCCGCCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG
ATGATCGCTGCCATCAGCCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC
AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTCTGAAGCTTGAAGGT
AAGCCTATCCCTAACCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC
CATCACCATTGA

FIG. 5

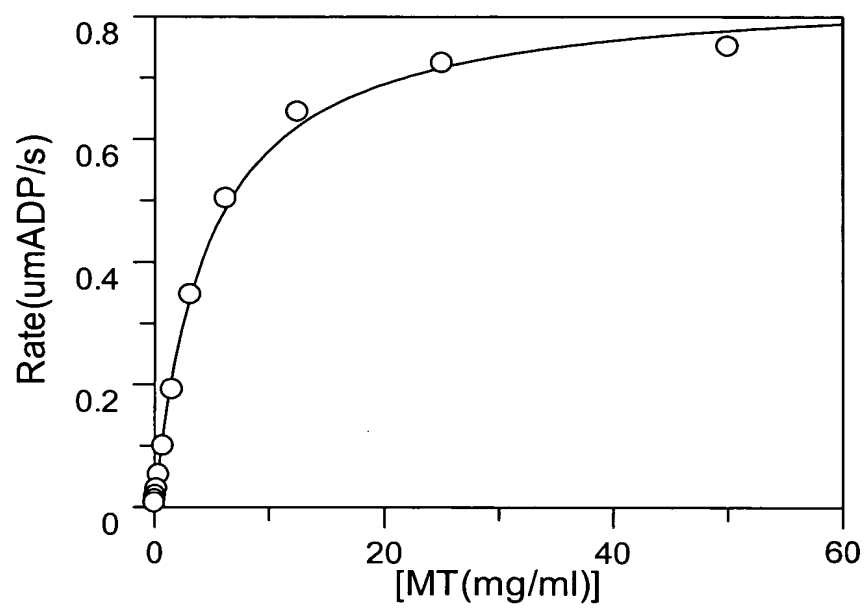


FIG. 6

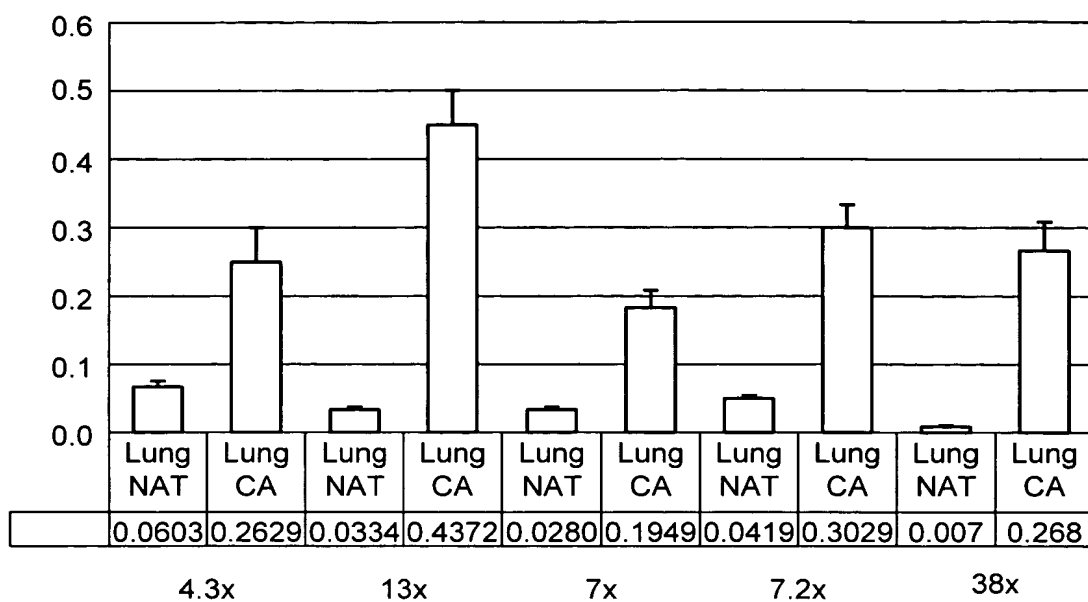


FIG. 7A

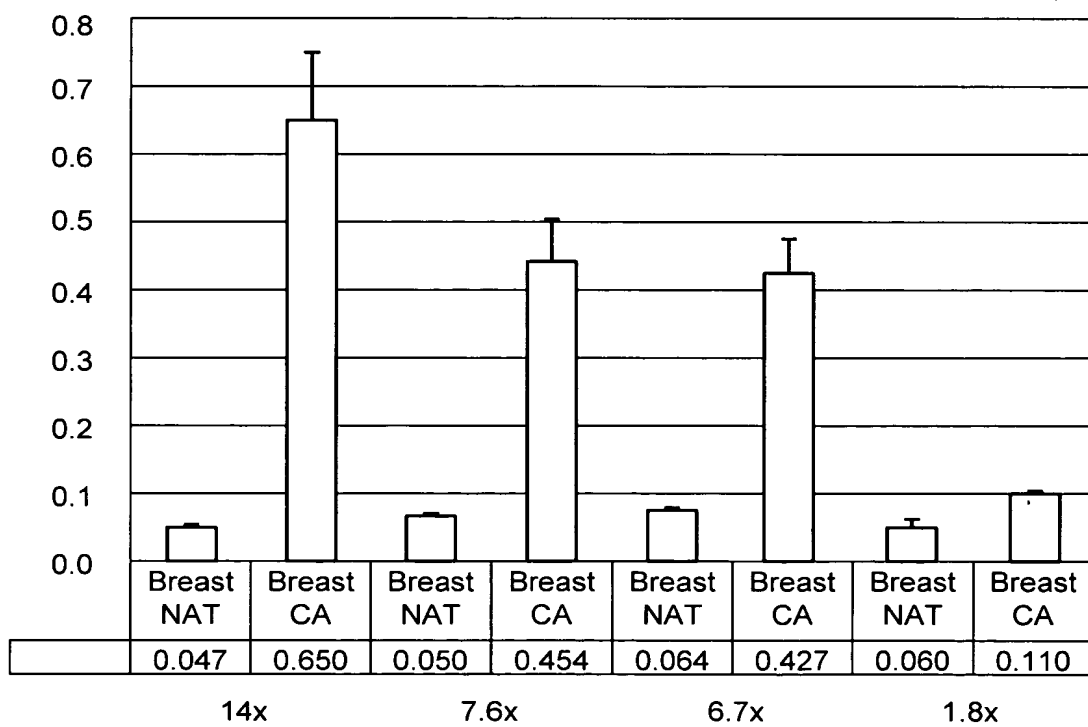


FIG. 7B

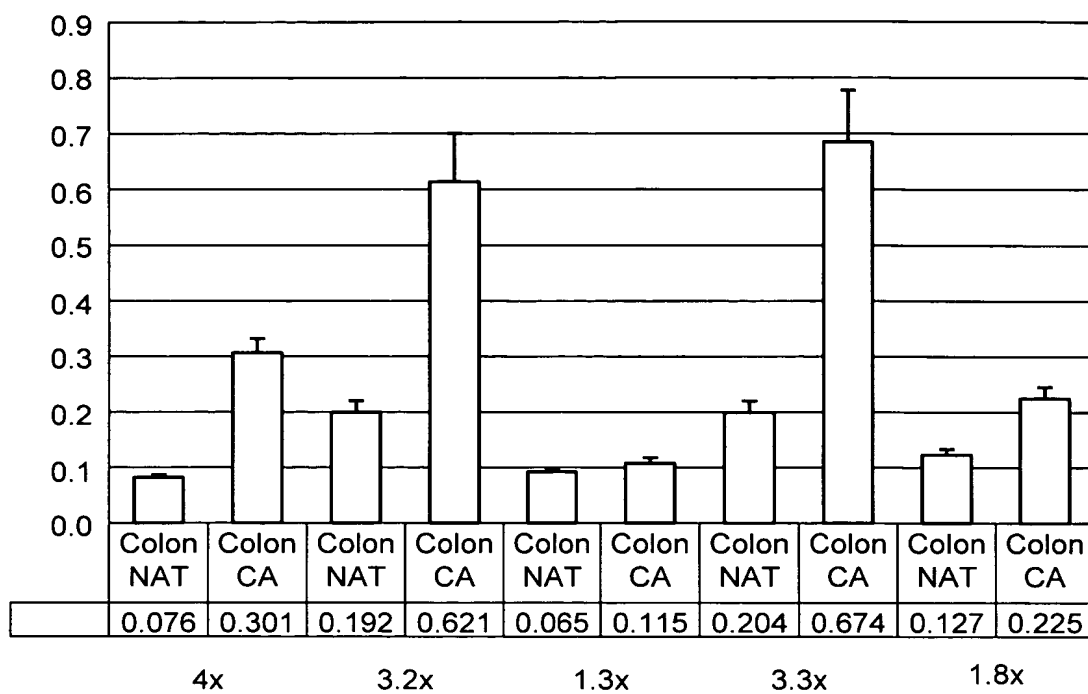


FIG. 7C

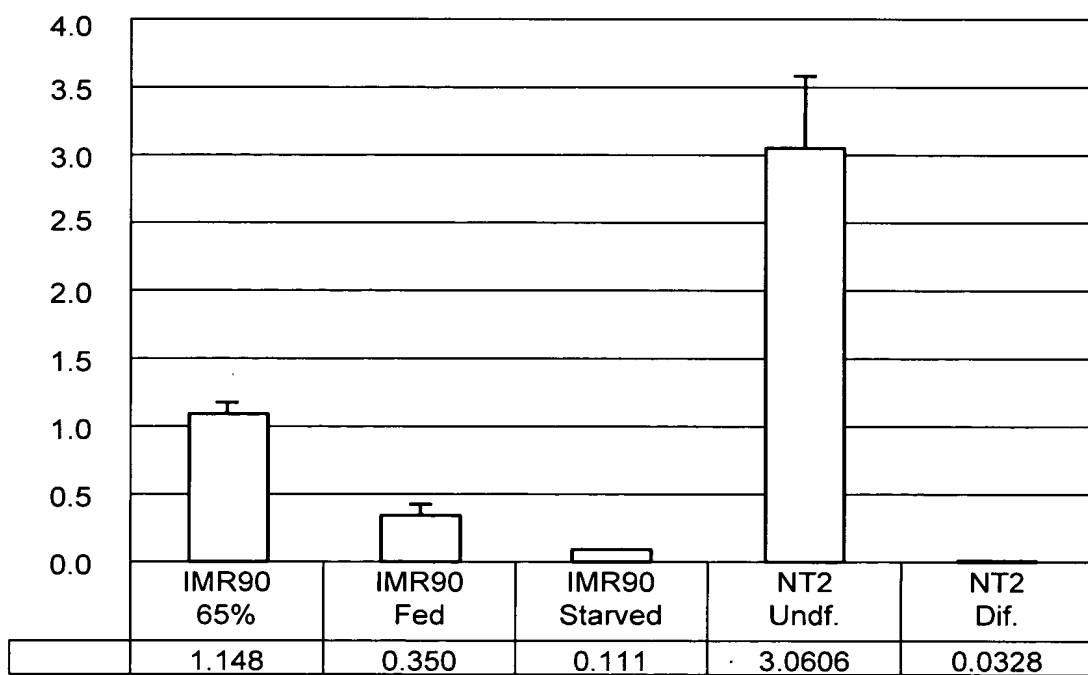


FIG. 7D